AMENDMENTS TO THE SPECIFICATION:

Please cancel the paragraph on page 2, line 7, to page 3, line 2, and replace it with the following paragraph:

--The complete Tat protein is made up of 101 amino acids, residues 1-72 being coded by a first exon and residues 73-101 being coded by a second exon. The Tat protein is strongly conserved. A truncated form of 86 amino acids, which does not correspond to the native form, exists in a few laboratory strains obtained after culture passages. This truncated form is due to the introduction of a stop codon at position 87 during the culture passages, but more than 90% of the Tat proteins studied maintain the configuration of 101 amino acids. Although amino acids 87-101 could not contribute greatly to ex vivo propagation, their conservation in the natural isolates of HIV-1 which replicate is an indication of their biological importance. HIV-1's native Tat protein of 101 amino acids is made up of five physical domains, but the molecular mechanism by which it acts has not yet been completely explained. Briefly, these five domains are described in the publication of Jeang, K. T et al. (18). In this publication, domain 1 corresponds to amino acids 1-20 which are rich in acid residues, domain 2 corresponds to amino acids 21-40 which are rich in cysteine residues (7 cysteine residues, 6 of which are very strongly conserved), domain 3 corresponds to amino acids 41-48 and contains the RKGLGI motif (SEQ ID NO: 109) common to HIV-1, HIV-2 and SIV, domain 4 corresponds to amino acids 49-72 and contains a basic RKKRRQRRR motif (SEQ ID NO: 110) and domain 5 corresponds to amino acids 73-101 and comprises an RGD motif. The role of domain 1 has not yet been explained. It has only been shown that changes in a

single amino acid in this domain were well tolerated and did not alter the functionality of the Tat protein. One hypothesis put forward is that domain 1 could be involved in transactivation. Changing six cysteines out of the seven in domain 2 suppresses the functionality of the Tat protein. This domain is important for transactivation. The role of domain 3 has not been elucidated. Domain 4 confers the properties of Tat fixation on the TAR RNA and is important for nuclear localization as well as for transcellular transport of the Tat protein. Domain 5 would also be involved in the transcellular transport of the Tat protein.--

Please cancel the paragraph on page 12, lines 11-14, and replace it with the following paragraph:

--Such antibodies are selected by testing and eliminating those which possess an affinity for a peptide corresponding to domain D1 of Tat, containing at least the sequence EPVDPKLEPWKHPGS (residues 2-16), (SEQ ID NO: 111), for example in an Elisa format test.--

Please cancel the paragraph on page 15, lines 16-18, and replace it with the following paragraph:

--Figure 2 represents the alignment of the protein sequence of the Tat protein of the strain ACH320.2A.2.1 (SEQ ID NO: 1) and of the protein sequences of the mutated Tat proteins of the invention (SEQ ID NOS 2-108).--

Please cancel the paragraph on page 17, lines 1-6, and replace it with the following paragraph:

--The double mutant R52L-R55L was generated using the following primers for single mutagenesis containing the two mutations:

R52L-R55L (M5')
5'-GGCAGGAAGCTTAGACAGCTGCGAAGATC-3' (SEQ ID NO: 112)

R52L-R55L (M3')
5'-GATCTTCGCAGCTGTCTAAGCTTCTTCCTGCC-3' (SEQ ID NO: 113)--

Please delete the Table 1 on page 23, and replace it with the following table:

End primers, 1st cycle	Sequence	SEQ ID NO:
E5′	5′- GAA TTC ATG GAG CCA GTA GAT C- 3′	114
E3′	5′- AGA TCT CTA ATC GAC CGG ATC- 3′	115
End primers, 2nd cycle		
EcoR I	5′- AAA GAA TTC ATG GAG CCA GTA GAT CC- 3′	116
E6854	5′- AAA GAT CTC TAA TCG ACC GGA TCT GTC TCT GTC TC- 3′	117
Sal I	5′- AAG TCG ACC TAA TCG ACC GGA TCT GTC TCT GTC TC- 3′	118
Internal primers		
W11F (M5′)	5′- CCA GTA GAT CCT AAA CTA GAG CCC TTC AAG CAT CCA G-3′	119
C27S (M5′)	5′- ACA ATT GCT ATT CGA AAA AGT G- 3′	120
C27S (M3′)	5′- CAC TTT TTC GAA TAG CAA TTG T- 3′	121
K50R (M5′)	5′- ATC TCA TAT GGC AGG CGG AAG -3′	122
K50R (M3′)	5′- CTT CCG CCT GCC ATA TGA GAT -3′	123
K51T (M5′)	5′- GGC AGG AAG ACC CGG AGA CAG C- 3′	124
K51T (M3′)	5′- GCT GTC TCC GGG TCT TCC TGC C- 3′	125
R52L (M5′)	5′- GGC AGG AAG AAG CTT AGA CAG CGA CGA AGA TC - 3′	126
R52L (M3′)	5′- GAT CTT CGT CGC TGT CTA AGC TTC TTC CTG CC- 3′	127
R55L (M5′)	5′- GGC AGG AAG AAG CGG AGA CAG CTG CGA AGA TC- 3′	128
R55L (M3′)	5′- GAT CTT CGC AGC TGT CTC CGC TTC TTC CTG CC- 3′	129
R57L (M5′)	5′- GAC AGC GAC GAC TAT CTC CTC AAG AC -3′	130
R57L (M3′)	5′- GTC TTG AGG AGA TAG TCG TCG CTG TC- 3′	131
G79A (M5′)	5′- CAG CCC CGA GCG GAT CCG ACA GG- 3′	132
G79A (M3′)	5′- CCT GTC GGA TCC GCT CGG GGC TG- 3′	133
K89L (M3′)	5′- CTG TCT CTG TCT CTC TCT CCA CCT TAA GCT TCG ATT CC- 3′	134
E92Q (M3′)	5′- CTG TCT CTG TCT CTC TTT GCA CCT TCT TCT TCG AAT CC- 3′	135

R52L-R55L(M5′)	5′- GGC AGG AAG AAG CTT AGA CAG CTG CGA AGA TC -3′	136
R52L-R55L (M3′)	5′- GAT CTT CGC AGC TGT CTA AGC TTC TTC CTG CC -3′	137
R55L-R57L (M5′)	5′- GAA GCG GAG ACA GCT GCG ACT ATC TCC TCA AGA C -3′	138
R55L-R57L (M3′)	5′- GTC TTG AGG AGA TAG TCG CAG CTG TCT CCG CTT C -3′	139
S58A (M5')	5'- GAC AGC GAC GAA GAG CAC CTC AAG ACA GT -3'	140
S58A (M3')	5'- ACT GTC TTG AGG TGC TCT TCG TCG CTG TC -3'	141

TABLE 1